

Supplementary Table 1.

The extended Cx43 interactome retrieved and constructed using the STRING database version 10.0 (<http://string-db.org>), using a high confidence score prediction setting (>0.7) as viewed in Supplementary Figure 1. In bold are hits from the highest prediction setting of (>0.9) as viewed in Figure 4.

PROTEIN	STRING ID	ANNOTATION	SCORE
TJP1	9606.ENSP00000281537	tight junction protein 1; The N-terminal may be involved in transducing a signal required for tight junction assembly, while the C-terminal may have specific properties of tight junctions. The alpha domain might be involved in stabilizing junctions. Plays a role in the regulation of cell migration by targeting CDC42BPB to the leading edge of migrating cells	0.998
UBC	9606.ENSP00000344818	ubiquitin C	0.995
CDH2	9606.ENSP00000269141	cadherin 2, type 1, N-cadherin (neuronal); Cadherins are calcium-dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. CDH2 may be involved in neuronal recognition mechanism. In hippocampal neurons, may regulate dendritic spine density (By similarity)	0.994
MAPK7	9606.ENSP00000311005	mitogen-activated protein kinase 7; Plays a role in various cellular processes such as proliferation, differentiation and cell survival. The upstream activator of MAPK7 is the MAPK kinase MAP2K5. Upon activation, it translocates to the nucleus and phosphorylates various downstream targets including MEF2C. EGF activates MAPK7 through a Ras- independent and MAP2K5-dependent pathway. May have a role in muscle cell differentiation. May be important for endothelial function and maintenance of blood vessel integrity.	0.994
SRC	9606.ENSP00000350941	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian); Non-receptor protein tyrosine kinase which is activated following engagement of many different classes of cellular receptors including immune response receptors, integrins and other adhesion receptors, receptor protein tyrosine kinases, G protein- coupled receptors as well as cytokine receptors. Participates in signaling pathways that control a diverse spectrum of biological activities including gene transcription, immune response, cell adhesion, cell cycle progression, apoptosis, migration, and transformation.	0.99
JUN	9606.ENSP00000360266	jun proto-oncogene; Transcription factor that recognizes and binds to the enhancer heptamer motif 5'-TGA[CG]TCA-3'. Promotes activity of NR5A1 when phosphorylated by HIPK3 leading to increased steroidogenic gene expression upon cAMP signaling pathway stimulation	0.989
MAPK1	9606.ENSP00000215832	mitogen-activated protein kinase 1; Serine/threonine kinase which acts as an essential component of the MAP kinase signal transduction pathway. MAPK1/ERK2 and MAPK3/ERK1 are the 2 MAPKs which play an important role in the MAPK/ERK cascade. They participate also in a signaling cascade initiated by activated KIT and KITLG/SCF. Depending on the cellular context, the MAPK/ERK cascade mediates diverse biological functions such as cell growth, adhesion, survival and differentiation through the regulation of transcription, translation, cytoskeletal rearrangements.	0.985
UBQLN4	9606.ENSP00000357292	ubiquilin 4; Plays a role in the regulation of proteasomal protein degradation. Depending on the case, may promote or inhibit proteasomal protein degradation	0.985

MAPK3	9606.ENSP00000263025	mitogen-activated protein kinase 3; Serine/threonine kinase which acts as an essential component of the MAP kinase signal transduction pathway. MAPK1/ERK2 and MAPK3/ERK1 are the 2 MAPKs which play an important role in the MAPK/ERK cascade. They participate also in a signaling cascade initiated by activated KIT and KITLG/SCF. Depending on the cellular context, the MAPK/ERK cascade mediates diverse biological functions such as cell growth, adhesion, survival and differentiation through the regulation of transcription, translation, cytoskeletal rearrangements.	0.981
CTNNB1	9606.ENSP00000344456	catenin (cadherin-associated protein), beta 1, 88kDa; Key downstream component of the canonical Wnt signaling pathway. In the absence of Wnt, forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. In the presence of Wnt ligand, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to activate Wnt responsive genes. Involved in the regulation [...]	0.952
FOS	9606.ENSP00000306245	FBJ murine osteosarcoma viral oncogene homolog; Nuclear phosphoprotein which forms a tight but non-covalently linked complex with the JUN/AP-1 transcription factor. In the heterodimer, FOS and JUN/AP-1 basic regions each seems to interact with symmetrical DNA half sites. On TGF-beta activation, forms a multimeric SMAD3/SMAD4/JUN/FOS complex at the AP1/SMAD-binding site to regulate TGF-beta-mediated signaling. Has a critical function in regulating the development of cells destined to form and maintain the skeleton.	0.948
NOV	9606.ENSP00000259526	nephroblastoma overexpressed; Immediate-early protein likely to play a role in cell growth regulation (By similarity)	0.946
AKT1	9606.ENSP00000270202	v-akt murine thymoma viral oncogene homolog 1; AKT1 is one of 3 closely related serine/threonine-protein kinases (AKT1, AKT2 and AKT3) called the AKT kinase, and which regulate many processes including metabolism, proliferation, cell survival, growth and angiogenesis. This is mediated through serine and/or threonine phosphorylation of a range of downstream substrates. Over 100 substrate candidates have been reported so far, but for most of them, no isoform specificity has been reported. AKT is responsible of the regulation of glucose uptake by mediating insulin-induced translocation	0.93
KIAA1432	9606.ENSP00000416696	KIAA1432	0.929
CTNND1	9606.ENSP00000382004	catenin (cadherin-associated protein), delta 1	0.927
PRKCG	9606.ENSP00000263431	protein kinase C, gamma; Calcium-activated, phospholipid- and diacylglycerol (DAG)-dependent serine/threonine-protein kinase that plays diverse roles in neuronal cells and eye tissues, such as regulation of the neuronal receptors GRIA4/GLUR4 and GRIN1/NMDAR1, modulation of receptors and neuronal functions related to sensitivity to opiates, pain and alcohol, mediation of synaptic function and cell survival after ischemia, and inhibition of gap junction activity after oxidative stress.	0.925
PKP2	9606.ENSP00000070846	plakophilin 2; May play a role in junctional plaques	0.925

EPS15	9606.ENSP00000360798	epidermal growth factor receptor pathway substrate 15; Involved in cell growth regulation. May be involved in the regulation of mitogenic signals and control of cell proliferation. Involved in the internalization of ligand-inducible receptors of the receptor tyrosine kinase (RTK) type, in particular EGFR. Plays a role in the assembly of clathrin-coated pits (CCPs). Seems to be involved in CCPs maturation including invagination or budding. Involved in endocytosis of integrin beta- 1 (ITGB1) and transferrin receptor (TFR); internalization of ITGB1 as DAB2-dependent cargo	0.924
LEF1	9606.ENSP00000265165	lymphoid enhancer-binding factor 1; Participates in the Wnt signaling pathway. Activates transcription of target genes in the presence of CTNNB1 and EP300. May play a role in hair cell differentiation and follicle morphogenesis. TLE1, TLE2, TLE3 and TLE4 repress transactivation mediated by LEF1 and CTNNB1. Regulates T-cell receptor alpha enhancer function. Binds DNA in a sequence-specific manner. PIAG antagonizes both Wnt-dependent and Wnt-independent activation by LEF1 (By similarity). Isoform 3 lacks the CTNNB1 interaction domain and may be an antagonist for Wnt signaling.	0.921
CSNK1D	9606.ENSP00000324464	casein kinase 1, delta; Essential serine/threonine-protein kinase that regulates diverse cellular growth and survival processes including Wnt signaling, DNA repair and circadian rhythms. It can phosphorylate a large number of proteins. Casein kinases are operationally defined by their preferential utilization of acidic proteins such as caseins as substrates. Phosphorylates connexin-43/GJA1, MAP1A, SNAPIN, MAPT/TAU, TOP2A, DCK, HIF1A, EIF6, p53/TP53, DVL2, DVL3, ESR1, AIB1/NCOA3, DNMT1, PKD2, YAP1, PER1 and PER2.	0.916
JUNB	9606.ENSP00000303315	jun B proto-oncogene; Transcription factor involved in regulating gene activity following the primary growth factor response. Binds to the DNA sequence 5'-TGA[CG]TCA-3'	0.912
FGF2	9606.ENSP00000264498	fibroblast growth factor 2 (basic)	0.909
CTNNA1	9606.ENSP00000304669	catenin (cadherin-associated protein), alpha 1, 102kDa; Associates with the cytoplasmic domain of a variety of cadherins. The association of catenins to cadherins produces a complex which is linked to the actin filament network, and which seems to be of primary importance for cadherins cell-adhesion properties. Can associate with both E- and N-cadherins. Originally believed to be a stable component of E-cadherin/catenin adhesion complexes and to mediate the linkage of cadherins to the actin cytoskeleton at adherens junctions.	0.908
EDN1	9606.ENSP00000368683	endothelin 1; Endothelins are endothelium-derived vasoconstrictor peptides	0.908
SGSM3	9606.ENSP00000248929	small G protein signaling modulator 3; May play a cooperative role in NF2-mediated growth suppression of cells	0.907
DCTN1	9606.ENSP00000354791	dynactin 1	0.905
TJP2	9606.ENSP00000438262	tight junction protein 2	0.903
MAPRE1	9606.ENSP00000364721	microtubule-associated protein, RP/EB family, member 1; Binds to the plus end of microtubules and regulates the dynamics of the microtubule cytoskeleton. Promotes cytoplasmic microtubule nucleation and elongation. May be involved in spindle function by stabilizing microtubules and anchoring them at centrosomes. May play a role in cell migration	0.9

VCL	9606.ENSP00000211998	vinculin; Actin filament (F-actin)-binding protein involved in cell-matrix adhesion and cell-cell adhesion. Regulates cell- surface E-cadherin expression and potentiates mechanosensing by the E-cadherin complex. May also play important roles in cell morphology and locomotion	0.896
IGF1	9606.ENSP00000302665	insulin-like growth factor 1 (somatomedin C); The insulin-like growth factors, isolated from plasma, are structurally and functionally related to insulin but have a much higher growth-promoting activity. May be a physiological regulator of [1-14C]-2-deoxy-D-glucose (2DG) transport and glycogen synthesis in osteoblasts. Stimulates glucose transport in rat bone-derived osteoblastic (PyMS) cells and is effective at much lower concentrations than insulin, not only regarding glycogen and DNA synthesis but also with regard to enhancing glucose uptake	0.889
GJA5	9606.ENSP00000271348	gap junction protein, alpha 5, 40kDa; One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low MW diffuse from one cell to a neighboring cell	0.888
GDF9	9606.ENSP00000296875	growth differentiation factor 9; Required for ovarian folliculogenesis. Promotes primordial follicle development. Stimulates granulosa cell proliferation. Promotes cell transition from G0/G1 to S and G2/M phases, through an increase of CCND1 and CCNE1 expression, and RB1 phosphorylation. It regulates STAR expression and cAMP-dependent progesterone release in granulosa and thecal cells. Attenuates the suppressive effects of activin A on STAR expression and progesterone production by increasing the expression of inhibin B. It suppresses FST and FSTL3 production in granulosa-lutein cells	0.88
PTH	9606.ENSP00000282091	parathyroid hormone; PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion. Stimulates [1-14C]-2- deoxy-D-glucose (2DG) transport and glycogen synthesis in osteoblastic cells	0.878
TGFB1	9606.ENSP00000221930	transforming growth factor, beta 1; Multifunctional protein that controls proliferation, differentiation and other functions in many cell types. Many cells synthesize TGFB1 and have specific receptors for it. It positively and negatively regulates many other growth factors. It plays an important role in bone remodeling as it is a potent stimulator of osteoblastic bone formation, causing chemotaxis, proliferation and differentiation in committed osteoblasts	0.877
NEDD4	9606.ENSP00000345530	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase	0.875
MYOCD	9606.ENSP00000401678	myocardin; Smooth muscle cells (SM) and cardiac muscle cells-specific transcriptional factor which uses the canonical single or multiple CArG boxes DNA sequence. Acts as a cofactor of serum response factor (SRF) with the potential to modulate SRF-target genes. Plays a crucial role in cardiogenesis and differentiation of the smooth muscle cell lineage (myogenesis) (By similarity)	0.865
CXCL12	9606.ENSP00000379140	chemokine (C-X-C motif) ligand 12	0.865
F2	9606.ENSP00000308541	coagulation factor II (thrombin); Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and, in complex with thrombomodulin, protein C. Functions in blood homeostasis, inflammation and wound healing	0.864

MAPK8	9606.ENSP00000353483	mitogen-activated protein kinase 8; Serine/threonine-protein kinase involved in various processes such as cell proliferation, differentiation, migration, transformation and programmed cell death. Extracellular stimuli such as proinflammatory cytokines or physical stress stimulate the stress-activated protein kinase/c-Jun N-terminal kinase (SAP/JNK) signaling pathway. In this cascade, two dual specificity kinases MAP2K4/MKK4 and MAP2K7/MKK7 phosphorylate and activate MAPK8/JNK1.	0.86
TBX2	9606.ENSP00000240328	T-box 2; Involved in the transcriptional regulation of genes required for mesoderm differentiation. Probably plays a role in limb pattern formation. Acts as a negative regulator of PML function in cellular senescence	0.859
CDK1	9606.ENSP00000378699	cyclin-dependent kinase 1; Plays a key role in the control of the eukaryotic cell cycle by modulating the centrosome cycle as well as mitotic onset; promotes G2-M transition, and regulates G1 progress and G1-S transition via association with multiple interphase cyclins. Required in higher cells for entry into S-phase and mitosis. Phosphorylates PARVA/actopaxin, APC, AMPH, APC, BARD1, Bcl-xL/BCL2L1, BRCA2, CALD1, CASP8, CDC7, CDC20, CDC25A, CDC25C, CC2D1A, CSNK2 proteins/CKII, FZR1/CDH1, CDK7, CEBPB, CHAMP1, DMD/dystrophin, EEF1 proteins/EF-1, EZH2, KIF11/EG5, EGFR, FANCG, FOS, GFAP, G [...]	0.854
HRAS	9606.ENSP00000309845	v-Ha-ras Harvey rat sarcoma viral oncogene homolog; Ras proteins bind GDP/GTP and possess intrinsic GTPase activity	0.854
CRH	9606.ENSP00000276571	corticotropin releasing hormone; This hormone from hypothalamus regulates the release of corticotropin from pituitary gland	0.854
SLC9A1	9606.ENSP00000263980	solute carrier family 9, subfamily A (NHE1, cation proton antiporter 1), member 1; Involved in pH regulation to eliminate acids generated by active metabolism or to counter adverse environmental conditions. Major proton extruding system driven by the inward sodium ion chemical gradient. Plays an important role in signal transduction	0.854
PRKCA	9606.ENSP00000408695	protein kinase C, alpha; Calcium-activated, phospholipid- and diacylglycerol (DAG)-dependent serine/threonine-protein kinase that is involved in positive and negative regulation of cell proliferation, apoptosis, differentiation, migration and adhesion, tumorigenesis, cardiac hypertrophy, angiogenesis, platelet function and inflammation, by directly phosphorylating targets such as RAF1, BCL2, CSPG4, TNNT2/CTNT, or activating signaling cascade involving MAPK1/3 (ERK1/2) and RAP1GAP. Involved in cell proliferation and cell growth arrest	0.85
BMP7	9606.ENSP00000379204	bone morphogenetic protein 7; Induces cartilage and bone formation. May be the osteoinductive factor responsible for the phenomenon of epithelial osteogenesis. Plays a role in calcium regulation and bone homeostasis	0.85
DLG1	9606.ENSP00000345731	discs, large homolog 1 (Drosophila)	0.85
WNT3A	9606.ENSP00000284523	wingless-type MMTV integration site family, member 3A; Ligand for members of the frizzled family of seven transmembrane receptors. Wnt-3 and Wnt-3a play distinct roles in cell-cell signaling during morphogenesis of the developing neural tube	0.85
BAX	9606.ENSP00000293288	BCL2-associated X protein	0.846
SOST	9606.ENSP00000301691	sclerostin; Negative regulator of bone growth that acts through inhibition of Wnt signaling and bone formation	0.842
SPP1	9606.ENSP00000378517	secreted phosphoprotein 1	0.835

CAV3	9606.ENSP00000341940	caveolin 3; May act as a scaffolding protein within caveolar membranes. Interacts directly with G-protein alpha subunits and can functionally regulate their activity. May also regulate voltage-gated potassium channels. Plays a role in the sarcolemma repair mechanism of both skeletal muscle and cardiomyocytes that permits rapid resealing of membranes disrupted by mechanical stress	0.834
CAV2	9606.ENSP00000222693	caveolin 2; May act as a scaffolding protein within caveolar membranes. Interacts directly with G-protein alpha subunits and can functionally regulate their activity. Acts as an accessory protein in conjunction with CAV1 in targeting to lipid rafts and driving caveolae formation. The Ser-36 phosphorylated form has a role in modulating mitosis in endothelial cells. Positive regulator of cellular mitogenesis of the MAPK signaling pathway. Required for the insulin-stimulated nuclear translocation and activation of MAPK1 and STAT3, and the subsequent regulation of cell cycle progression	0.833
CNTF	9606.ENSP00000355370	ciliary neurotrophic factor; CNTF is a survival factor for various neuronal cell types. Seems to prevent the degeneration of motor axons after axotomy	0.832
TOMM20	9606.ENSP00000355566	translocase of outer mitochondrial membrane 20 homolog (yeast); Central component of the receptor complex responsible for the recognition and translocation of cytosolically synthesized mitochondrial preproteins. Together with TOM22 functions as the transit peptide receptor at the surface of the mitochondrion outer membrane and facilitates the movement of preproteins into the TOM40 translocation pore (By similarity)	0.828
AGT	9606.ENSP00000355627	angiotensinogen (serpin peptidase inhibitor, clade A, member 8); Essential component of the renin-angiotensin system (RAS), a potent regulator of blood pressure, body fluid and electrolyte homeostasis	0.827
NOS1	9606.ENSP00000337459	nitric oxide synthase 1 (neuronal); Produces nitric oxide (NO) which is a messenger molecule with diverse functions throughout the body. In the brain and peripheral nervous system, NO displays many properties of a neurotransmitter. Probably has nitrosylase activity and mediates cysteine S-nitrosylation of cytoplasmic target proteins such SRR	0.826
FGF9	9606.ENSP00000371790	fibroblast growth factor 9 (glia-activating factor); Plays an important role in the regulation of embryonic development, cell proliferation, cell differentiation and cell migration. May have a role in glial cell growth and differentiation during development, gliosis during repair and regeneration of brain tissue after damage, differentiation and survival of neuronal cells, and growth stimulation of glial tumors	0.824
KAT2B	9606.ENSP00000263754	K(lysine) acetyltransferase 2B; Functions as a histone acetyltransferase (HAT) to promote transcriptional activation. Has significant histone acetyltransferase activity with core histones (H3 and H4), and also with nucleosome core particles. Inhibits cell-cycle progression and counteracts the mitogenic activity of the adenoviral oncoprotein E1A. In case of HIV-1 infection, it is recruited by the viral protein Tat. Regulates Tat's transactivating activity and may help inducing chromatin remodeling of proviral genes	0.821
HSPA8	9606.ENSP00000227378	heat shock 70kDa protein 8; Acts as a repressor of transcriptional activation. Inhibits the transcriptional coactivator activity of CITED1 on Smad-mediated transcription. Chaperone. Component of the PRP19- CDC5L complex that forms an integral part of the spliceosome and is required for activating pre-mRNA splicing. May have a scaffolding role in the spliceosome assembly as it contacts all other components of the core complex	0.82

GJD2	9606.ENSP00000290374	gap junction protein, delta 2, 36kDa; One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low MW diffuse from one cell to a neighboring cell (By similarity)	0.817
TUBB2A	9606.ENSP00000369703	tubulin, beta 2A class IIa; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.815
TUBB3	9606.ENSP00000451560	tubulin, beta 3 class III; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.815
TUBA1B	9606.ENSP00000336799	tubulin, alpha 1b; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.813
TUBA1C	9606.ENSP00000301072	tubulin, alpha 1c; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.812
ERP29	9606.ENSP00000261735	endoplasmic reticulum protein 29; Does not seem to be a disulfide isomerase. Plays an important role in the processing of secretory proteins within the endoplasmic reticulum (ER), possibly by participating in the folding of proteins in the ER	0.812
TUBA3E	9606.ENSP00000318197	tubulin, alpha 3e; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.811
EHD1	9606.ENSP00000320516	EH-domain containing 1; Acts in early endocytic membrane fusion and membrane trafficking of recycling endosomes	0.807
TUBA1A	9606.ENSP00000301071	tubulin, alpha 1a; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.806
WNT2	9606.ENSP00000265441	wingless-type MMTV integration site family member 2; Ligand for members of the frizzled family of seven transmembrane receptors. Probable developmental protein. May be a signaling molecule which affects the development of discrete regions of tissues. Is likely to signal over only few cell diameters	0.806
TUBA4A	9606.ENSP00000248437	tubulin, alpha 4a; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.805
TUBB6	9606.ENSP00000318697	tubulin, beta 6 class V; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.802
CTTNBP2 NL	9606.ENSP00000271277	CTTNBP2 N-terminal like	0.802
TUBA3C	9606.ENSP00000382982	tubulin, alpha 3c; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.801
TUBB4A	9606.ENSP00000264071	tubulin, beta 4A class IVa; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.801

MRVI1	9606.ENSP00000412130	murine retrovirus integration site 1 homolog; Plays a role as NO/PRKG1-dependent regulator of IP3- induced calcium release; its phosphorylation by PRKG1 inhibits bradykinin and IP3-induced calcium release from intracellular stores. Recruits PRKG1 to the endoplasmic reticulum and may mediate the assembly of PRKG1 and ITPR1 in a macrocomplex. Involved in PRKG1 signaling cascade leading to inhibition of platelet activation and aggregation. Mediates also NO-dependent inhibition of calcium signaling in gastrointestinal smooth muscle contributing to NO-dependent relaxation	0.801
PTPRA	9606.ENSP00000369756	protein tyrosine phosphatase, receptor type, A	0.8
NPM3	9606.ENSP00000359128	nucleophosmin/nucleoplasmin 3; May act as a chaperone	0.8
TUBB4B	9606.ENSP00000341289	tubulin, beta 4B class IVb; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.8
GHRL	9606.ENSP00000335074	ghrelin/obestatin prepropeptide; Ghrelin is the ligand for growth hormone secretagogue receptor type 1 (GHSR). Induces the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation	0.8
CNTNAP3	9606.ENSP00000297668	contactin associated protein-like 3	0.8
TUBB2B	9606.ENSP00000259818	tubulin, beta 2B class IIb; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity). TUBB2B is implicated in neuronal migration	0.8
TUBB1	9606.ENSP00000217133	tubulin, beta 1 class VI; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha chain (By similarity)	0.8
CCNE1	9606.ENSP00000262643	cyclin E1; Essential for the control of the cell cycle at the G1/S (start) transition	0.799
IFNG	9606.ENSP00000229135	interferon, gamma; Produced by lymphocytes activated by specific antigens or mitogens. IFN-gamma, in addition to having antiviral activity, has important immunoregulatory functions. It is a potent activator of macrophages, it has antiproliferative effects on transformed cells and it can potentiate the antiviral and antitumor effects of the type I interferons (By similarity)	0.796
TNF	9606.ENSP00000398698	tumor necrosis factor	0.789
TAF2	9606.ENSP00000367406	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa; Transcription factor TFIID is one of the general factors required for accurate and regulated initiation by RNA polymerase II. TFIID is a multimeric protein complex that plays a central role in mediating promoter responses to various activators and repressors. It requires core promoter-specific cofactors for productive transcription stimulation. TAF2 stabilizes TFIID binding to core promoter	0.788

MFGE8	9606.ENSP00000268150	milk fat globule-EGF factor 8 protein; Plays an important role in the maintenance of intestinal epithelial homeostasis and the promotion of mucosal healing. Promotes VEGF-dependent neovascularization (By similarity). Contributes to phagocytic removal of apoptotic cells in many tissues. Specific ligand for the alpha-v/beta-3 and alpha-v/beta-5 receptors. Also binds to phosphatidylserine-enriched cell surfaces in a receptor-independent manner. Zona pellucida-binding protein which may play a role in gamete interaction. Binds specifically to rotavirus and inhibits its replication	0.782
KCNJ2	9606.ENSP00000243457	potassium inwardly-rectifying channel, subfamily J, member 2; Probably participates in establishing action potential waveform and excitability of neuronal and muscle tissues. Inward rectifier potassium channels are characterized by a greater tendency to allow potassium to flow into the cell rather than out of it. Their voltage dependence is regulated by the concentration of extracellular potassium; as external potassium is raised, the voltage range of the channel opening shifts to more positive voltages.	0.778
MAPK14	9606.ENSP00000229794	mitogen-activated protein kinase 14; Serine/threonine kinase which acts as an essential component of the MAP kinase signal transduction pathway. MAPK14 is one of the four p38 MAPKs which play an important role in the cascades of cellular responses evoked by extracellular stimuli such as proinflammatory cytokines or physical stress leading to direct activation of transcription factors. Accordingly, p38 MAPKs phosphorylate a broad range of proteins and it has been estimated that they may have approximately 200 to 300 substrates each. Some of the targets are downstream kinases which are a [...]	0.776
SEMA3D	9606.ENSP00000284136	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D; Induces the collapse and paralysis of neuronal growth cones. Could potentially act as repulsive cues toward specific neuronal populations. Binds to neuropilin (By similarity)	0.773
GJB1	9606.ENSP00000354900	gap junction protein, beta 1, 32kDa; One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low MW diffuse from one cell to a neighboring cell (By similarity)	0.757
GJB2	9606.ENSP00000372295	gap junction protein, beta 2, 26kDa; One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low MW diffuse from one cell to a neighboring cell (By similarity)	0.753
GJD3	9606.ENSP00000336832	gap junction protein, delta 3, 31.9kDa; One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low MW diffuse from one cell to a neighboring cell (By similarity)	0.741
GJA3	9606.ENSP00000241125	gap junction protein, alpha 3, 46kDa; One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low MW diffuse from one cell to a neighboring cell	0.739
KRAS	9606.ENSP00000256078	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog; Ras proteins bind GDP/GTP and possess intrinsic GTPase activity	0.737
DSC2	9606.ENSP00000280904	desmocollin 2; Component of intercellular desmosome junctions. Involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion. May contribute to epidermal cell positioning (stratification) by mediating differential adhesiveness between cells that express different isoforms	0.701

TSPO	9606.ENSPO0 000328973	translocator protein (18kDa); Responsible for the manifestation of peripheral-type benzodiazepine recognition sites and is most likely to comprise binding domains for benzodiazepines and isoquinoline carboxamides. May play a role in the transport of porphyrins and heme. Plays a role in the transport of cholesterol across mitochondrial membranes in steroidogenic cells (By similarity)	0.7
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